

Fig. 1
Jungkums

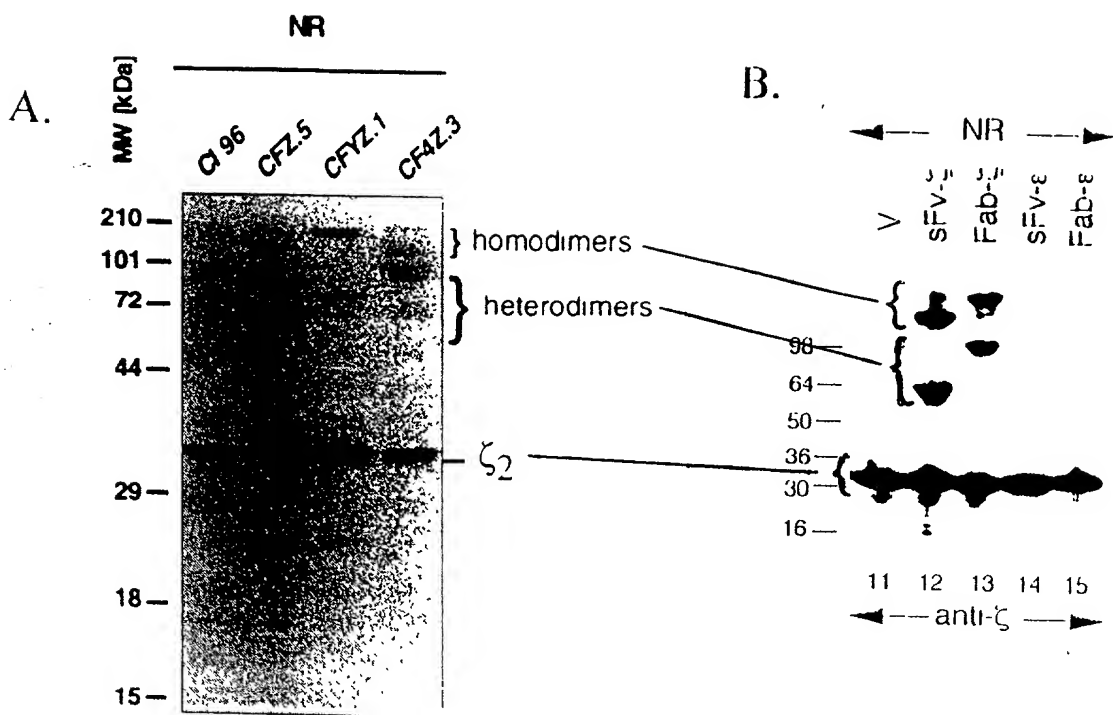


Fig. 2
Jungheun s

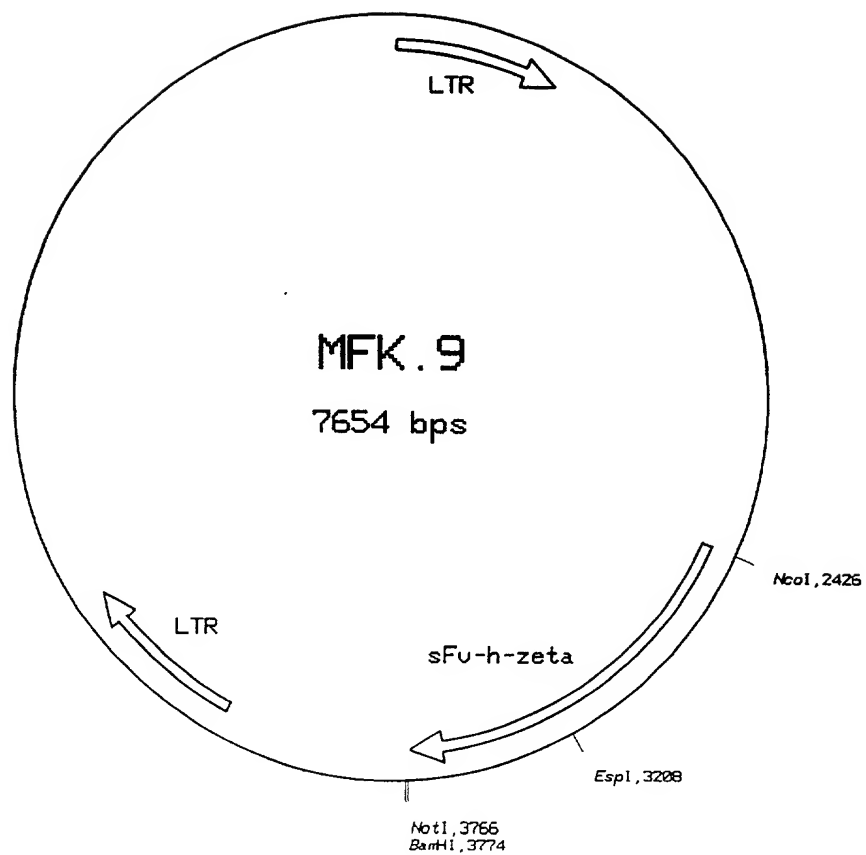


Fig. 3
Jinghan

NAME: BMB3.6-H-Ch 504 BPS DNA UPDATED 6/25/93
DESCRIPTION: Heavy chain leader and variable region of BMB3.6-h

* * * S E Q U E N C E * * *

1 TCACCATGAA CTTCGGGTTC AGCTTGATTT TCCTTGTCCT TGTTTTTAAAA GGTGTCCAGT
AGTGGTACTT GAAGCCCAAG TCGAACTAAA AGGAACAGGA ACAAATTTT CCACAGGTCA

61 GTGAAGTGGT GGTGGTGGAG TCTGGGGGAG GCTTCGTGAA GCCTGGAGGG TCCCTGAAAC
CACTTCACCA CCACCACCTC AGACCCCTC CGAAGCACTT CGGACCTCCC AGGGACTTTG

121 TCTCCTGTGC AGCCGCTGGA TTCACTTTCA GTAGATATGC CATGTCTTGG GTTCGCCAGA
AGAGGACACG TCGGCGACCT AAGTGAAAGT CATCTATACG GTACAGAACC CAAGCGGTCT

181 CTCCGGAGAA GAGGCTGGAG TGGGTGCGAA CCATAAGTAG TGGTGGTAGT CACACCTACT
GAGGCCTCTT CTCCGACCTC ACCCAGCGTT GGTATTCATC ACCACCATCA GTGTGGATGA

241 ATCCAGACAG TGTGAAGGGG CGATTCACCA TCTCCAGAGA CAATGCCAAG AACACCCTGT
TAGGTCTGTC AACTTCCCC GCTAAGTGGT AGAGGTCTCT GTTACGGTTC TTGTGGGACA

301 ACCTGCAAAT GAGCAGTCTG AGGTCTGAGG ACACGGCCAT ATATTACTGT GCAAGACCGG
TGGACGTTTA CTCGTCAGAC TCCAGACTCC TGTGCCGGTA TATAATGACA CGTTCTGGCC

361 GTTACGACAG GGGGGCCTGG TTTTTCGATG TCTGGGGCGC AGGGACCACG GTCACCGTCT
CAATGCTGTC CCCCCGGACC AAAAAGCTAC AGACCCCGCG TCCCTGGTGC CAGTGGCAGA

421 CCTCAGGTAA GTGTGTCAGG GTTTCACAAG AGGGACTAAA GACATGTCAG CTAATGTGTG
GGAGTCCATT CACACAGTCC CAAAGTGTTT TCCCTGATTT CTGTACAGTC GATTACACAC

481 ACTAATGGTA ATGTCACTAA GCTT
TGATTACCAT TACAGTGATT CGAA

Fig. 4A
Junkies

NAME: BMB3.6-L-Ch 483 BPS DNA UPDATED 6/25/93
DESCRIPTION: LIGHT CHAIN LEADER AND VARIABLE REGION OF bmb3.6 C

* * * S E Q U E N C E * * *

1 AGGGAAAGCT CGAAGATGGT TTTCACACCT CAGATACTTG GACTTATGCT TTTTGGATT
TCCCTTTCGA GCTTCTACCA AAAGTGTGGA GTCTATGAAC CTGAATACGA AAAAACCTAA
61 TCAGCCTCCA GAGGTGATAT TGTGCTAACT CAGTCTCCAG CCACCCTGTC TGTGACTCCA
AGTCGGAGGT CTCCACTATA ACACGATTGA GTCAGAGGTC GGTGGGACAG ACACTGAGGT
121 GGAGATAGCG TCAGTCTTTC CTGCAGGGCC AGCCAAATTA TTAGCAACAA CCTACACTGG
CCTCTATCGC AGTCAGAAAG GACGTCCCGG TCGGTTTAAT AATCGTTGTT GGATGTGACC
181 TATCAACAAA AATCACATGA GTCTCCAAGG CTTCTCATCA AGTATGCTTC CCAGTCCATC
ATAGTTGTTT TTAGTGTACT CAGAGGTTCC GAAGAGTAGT TCATACGAAG GGTGAGGTAG
241 TCTGGGATCC CCTCCAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTTAC TCTCAGTATC
AGACCCTAGG GGAGGTCCAA GTCACCGTCA CCTAGTCCCT GTCTAAAGTG AGAGTCATAG
301 AACAGTGTGG AGACTGAAGA TTTTGGGAATG TATTTCTGTC AACAGAGTAA CAGCTGGCCT
TTGTCACACC TCTGACTTCT AAAACCTTAC ATAAAGACAG TTGTCTCATT GTCGACCGGA
361 CTCACGTTTC GCTCGGGGAC AAAGCTGGAG ATCAAACGGC GTAAGTGTGT CAGGGTTTCA
GAGTGCAAGC CGAGCCCCTG TTTCGACCTC TAGTTTGCCG CATTACACA GTCCCAAAGT
421 CAAGAGGGAC TAAAGACATG TCAGCTAATG TGTGACTAAT GGTAATGTCA CTTGTCAGGA
GTTCTCCCTG ATTTCTGTAC AGTCGATTAC AACTGATTA CCATTACAGT GAACAGTCCT
481 TCC
AGG

Fig. 4B
Singhans

NAME: sFv MB3.6
 DESCRIPTION: Light chain leader plus sFv of MB3.6

*** S E Q U E N C E ***

1 GATATCAGAT CTCAGCTGTC TAGA CATATG GTTTTCACAC CTCAGATANN NNNNNNNNNN
 ORF → D I R S Q L S R H M V F T P Q I ? ? ? ?
 I S D L S C L D I W F S H L R ? ? ? ?
 Y Q I S A V - T Y G F H T S D ? ? ? ?
 leader ← V_L
 61 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNGGGAC AAAGCTGGAG
 ? ? ? ? ? ? ? ? ? ? ? ? ? ? ? ? G T K L E
 ? ? ? ? ? ? ? ? ? ? ? ? ? ? ? ? G Q S W
 ? ? ? ? ? ? ? ? ? ? ? ? ? ? ? ? D K A G
 V_L ← Linker
 121 ATCAAAGGTG GCTCAGGATC GGGTGGAGCC GGCTCTGGTG GCTCAGGATC GGAAGTGGTG
 I K G G S G S G G A G S G G S G S E V V
 R S K V A Q D R V E P A L V A Q D R K W
 D Q R W L R I G W S R L W W L R I G S G
 Linker → V_H
 181 GTGGTGGAGN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNACC
 V V E ? ? ? ? ? ? ? ? ? ? ? ? ? ? T
 W W W ? ? ? ? ? ? ? ? ? ? ? ? ? ? ?
 G G G ? ? ? ? ? ? ? ? ? ? ? ? ? ? ?
 V_H ← TCR E/h3
 241 ACGGTCACCG TCTCCAGT
 T V T V S S
 P R S P S P
 H G H R L Q

Fig. 4C
 J. J. J. J. J.

*** INPUT INFORMATION ***

FILE NAME : 3D8HCDNA.SEQ

SEQUENCE : 682BP; 153 A; 184 C; 173 G; 172 T.

*** SEQUENCE LIST ***

(DOUBLE)

10 20 30 40 50 60
5' TGAACACGGA CCCCTCACCA TGAAGTTCGG GCTCAGCTTG ATTTTCCTTG TCCTTGTTTT
3' ACTTGTGCCT GGGGAGTGGT ACTTGAAGCC CGAGTCGAAC TAAAAGGAAC AGGAACAAAA
70 80 90 100 110 120
AAAAGGTGTC CAGTGTGAAG TGAAGGTGGT GGAGTCTGGG GGAGGCTTAG TGAAGCCTGG
TTTTCCACAG GTCACACTTC ACTTCCACCA CCTCAGACCC CCTCCGAATC ACTTCGGACC
130 140 150 160 170 180
AGCGTCTCTG AAAGTCTCCT GTGCAGCCTC TGGATTCACT TTCAGTAACT ATGGCATGTC
TCGCAGAGAC TTTGAGAGGA CACGTCGGAG ACCTAAGTGA AAGTCATTGA TACCGTACAG
190 200 210 220 230 240
TTGGGTTCGC CAGACTTCAG ACAAGAGGCT GGAGTGGGTC GCATCCATTA GTAGTGGTGG
AACCCTAAGCG GTCTGAAGTC TGTTCTCCGA CCTCACCAG CGTAGGTAAT CATCACCACC
250 260 270 280 290 300
TGATAGCACC TTCTATGCAG ACAATGTAAA GGGCCGATTC ACCATCTCCA GAGAGAATGC
ACTATCGTGG AAGATACGTC TGTTACATTT CCCGGCTAAG TGGTAGAGGT CTCTCTTACG
310 320 330 340 350 360
CAAGAACACC CTGTACCTGC AAATGAGTAG TCTGAAGTCT GAGGACACGG CCTTGTATTA
GTTCTTGTGG GACATGGACG TTTACTCATC AGACTTCAGA CTCCTGTGCC GGAACATAAT
370 380 390 400 410 420
CTGTGCAAGA GACGATCTAT TTAAGTGGGG CCAAGGCACC ACTCTCACAG TCTCATCAGC
GACACGTTCT CTGCTAGATA AATTGACCCC GGTTCGCTGG TGAGAGTGTC AGAGTAGTCG
430 440 450 460 470 480
CAAAACAACA GCCCCATCGG TCTATCCACT GGCCCCTGTG TGTGGAGATA CAATTGGCTC
GTTTTGTTGT CGGGGTAGCC AGATAGGTGA CCGGGGACAC ACACCTCTAT GTTAACCGAG
490 500 510 520 530 540
CTCGGTGACT TTAGGATGCC TGGTCAAGGG TTATTTCTTT GAGCCAGTGA CCTTGACCTG
GAGCCACTGA AATCCTACGG ACCAGTTCCC AATAAAGGAA CTCGGTCACT GGAAGTGGAC
550 560 570 580 590 600
GAACTCTGGA TCCCTGTCCA GTGGTGTGCA CATCTTCCCA GCTGTCTTGC AGTCTGACCT
CTTGAGACCT AGGGACAGGT CACCACACGT GTAGAAGGGT CGACAGAACG TCAGACTGGA
610 620 630 640 650 660
CTACACCCTC AGCAGCTCAG TGAAGTGAAC CTCGAGCACC TGGCCCAGCC AGTCCATCAC
GATGTGGGAG TCGTCGAGTC ACTGACATTG GAGCTCGTGG ACCGGGTCGG TCAGGTAGTG
670 680
TTGCAATGTG GCCCACCCTG CA 3'
AACGTTACAC CGGGTGGGCC GT 5'

Fig. 4D
Junghans

*** INPUT INFORMATION ***

FILE NAME : 3D8LCDNA.SEQ

SEQUENCE : 729BP; 203 A; 177 C; 172 G; 177 T.

*** SEQUENCE LIST *** (DOUBLE)

	10	20	30	40	50	60
5'	CCGTTGCCGT	CGTGATGAGT	CCTGCCCAGT	TCCTGTTTCT	GTTAGTGCTC	TGGATTCAGG
3'	GGCAACGGCA	GCACTACTCA	GGACGGGTCA	AGGACAAAGA	CAATCACGAG	ACCTAAGTCC
	70	80	90	100	110	120
	AAACCAACGG	TGATGTTGTA	ATGACCCAGA	CTCCACTCAC	TTTGTGCGGT	ACCATTGGAC
	TTTGGTTGCC	ACTACAACAT	TACTGGGTCT	GAGGTGAGTG	AAACAGCCAA	TGGTAACCTG
	130	140	150	160	170	180
	AACCAGCCTC	TATCTCTTGC	AAGTCAAGTC	AGAGCCTCTT	ATATAGTAAT	GGAAAAACCT
	TTGGTCGGAG	ATAGAGAACG	TTCAGTTCAG	TCTCGGAGAA	TATATCATT	CCTTTTGGGA
	190	200	210	220	230	240
	ATTTGAATTG	GTTATTACAG	AGGCCAGGCC	AGTCTCCAAA	GCGCCTAATC	TATCTGGTGT
	TAAACTTAAC	CAATAATGTC	TCCGGTCCGG	TCAGAGGTTT	CGCGGATTAG	ATAGACCACA
	250	260	270	280	290	300
	CTAAACTGGA	CTCTGGAGTC	CCTGACAGGT	TCAGTGGCAG	TGGATCAGGA	ACAGATTTTA
	GATTTGACCT	GAGACCTCAG	GGACTGTCCA	AGTGACCGTC	ACCTAGTCCT	TGTCTAAAAT
	310	320	330	340	350	360
	CACTGAAAAT	CAGCAGAGTG	GAGGCTGAGG	ATTTGGGAGT	TTATTACTGC	GTGCAAGGTA
	GTGACTTTTA	GTCGTCTCAC	CTCCGACTCC	TAAACCCTCA	AATAATGACG	CACGTTCCAT
	370	380	390	400	410	420
	CACATTTTCC	TCACACGTTT	GGAGGGGGGA	CCAAGCTGGA	AATAAAAACG	GCTGATGCTG
	GTGTAAAAGG	AGTGTGCAAG	CCTCCCCCCT	GGTTCGACCT	TTATTTTGCC	CGACTACGAC
	430	440	450	460	470	480
	CACCAACTGT	ATCCATCTTC	CCACCATCCA	GTGAGCAGTT	AACATCTGGA	GGTGCCTCAG
	GTGGTTGACA	TAGGTAGAAG	GGTGGTAGGT	CACTCGTCAA	TTGTAGACCT	CCACGGAGTC
	490	500	510	520	530	540
	TCGTGTGCTT	CTTGAACAAC	TTCTACCCCA	AAGACATCAA	TGTCAAGTGG	AAGATTGATG
	AGCACACGAA	GAACCTGTTG	AAGATGGGGT	TTCTGTAGTT	ACAGTTCACC	TTCTAACTAC
	550	560	570	580	590	600
	GCAGTGAACG	ACAAAATGGC	GTCCTGAACA	GTTGGACTGA	TCAGGACAGC	AAAGACAGCA
	CGTCACTTGC	TGTTTTACCG	CAGGACTTGT	CAACCTGACT	AGTCCTGTCT	TTTCTGTCTG
	610	620	630	640	650	660
	CCTACAGCAT	GAGCAGCACC	CTCACGTTGA	CCAAGGACGA	GTATGAACGA	CATAACAGCT
	GGATGTCGTA	CTCGTCGTGG	GAGTGCAACT	GGTTCCTGCT	CATACTTGCT	GTATTGTCGA
	670	680	690	700	710	720
	ATACCTGTGA	GGCCACTCAC	AAGACATCAA	CTTCACCCAT	TGTCAAGAGC	TTCAACAGGA
	TATGGACACT	CCGGTGAGTG	TTCTGTAGTT	GAAGTGGGTA	ACAGTTCTCG	AAGTTGTCCT

ATGAGTGTT 3'
TACTCACAA 5'

Fig. 4E
Junghans

*** INPUT INFORMATION ***

FILE NAME : 4D4HCDNA.SEQ

SEQUENCE : 736BP; 170 A; 210 C; 186 G; 170 T.

*** SEQUENCE LIST ***

(DOUBLE)

10 20 30 40 50 60
5' ACTGACTCTA ACCATGGGAT GGAGATGGAT CTTTCTTTTC CTCCTGTCAG GAACTGCAGG
3' TGACTGAGAT TGGTACCCTA CCTCTACCTA GAAAGAAAAG GAGGACAGTC CTTGACGTCC
70 80 90 100 110 120
TGTCCATTGC CAGGTTTCAGC TGCAGCAGTC TGGACCTGAG CTGGTGAAGC CTGGGGCTTT
ACAGGTAACG GTCCAAGTCG ACGTCGTCAG ACCTGGACTC GACCACTTCG GACCCCGAAA
130 140 150 160 170 180
AGTGAAGATA TCCTGCAAGG CTTCTGGTTA CACCTTCACA AGCTACGATA TAAACTGGGT
TCACCTTCTAT AGGACGTTCC GAAGACCAAT GTGGAAGTGT TCGATGCTAT ATTTGACCCA
190 200 210 220 230 240
GAAGCAGAGG CCTGGACAGG GACTTGAGTG GATTGGATGG ATTTATCCTG GAGATGGTGG
CTTCGTCTCC GGACCTGTCC CTGAACTCAC CTAACCTACC TAAATAGGAC CTCTACCACC
250 260 270 280 290 300
TACTAATTAC AATGAGAAAT TCAAGGGCAA GGCCACACTG ACTGCAGACA AATCCTCCAG
ATGATTAATG TTA CTCTTTA AGTTC CCGTT CCGGTGTGAC TGACGTCTGT TTAGGAGGTC
310 320 330 340 350 360
CACAGCCTAC ATGCAGCTCA GTAGCCTGAC TTCTGAGAAC TCTGCAGTCT ATTTCTGTGC
GTGTCCGATG TACGTCGAGT CATCGGACTG AAGACTCTTG AGACGTCAGA TAAAGACACG
370 380 390 400 410 420
AAGAGGGGGT AACTTCCCTT CTTATGCTAT GGACTACTGG GGTCAAGGAA CCTCAGTCAC
TTCTCCCCCA TTGAAGGGAA GAATACGATA CCTGATGACC CCAGTTCCTT GGAGTCAGTG
430 440 450 460 470 480
CGTCTCCTCA GCCAAAACGA CACCCCCATC TGTCTATCCA CTGGCCCCCTG GATCTGCTGC
GCAGAGGAGT CGGTTTGTGCT GTGGGGGTAG ACAGATAGGT GACCGGGGAC CTAGACGACG
490 500 510 520 530 540
CCAAACTAAC TCCATGGTGA CCCC GGGATG CCTGGTCAAG GGCTATTTCC CTGAGCCAGT
GGTTTGATTG AGGTACCACT GGGGCCCTAC GGACCAGTTC CCGATAAAGG GACTCGGTCA
550 560 570 580 590 600
GACAGTGACC TGGAACTCTG GATCCCTGTC CAGCGGTGTG CACACCTTCC CAGCTGTCCT
CTGTCACTGG ACCTTGAGAC CTAGGGACAG GTCGCCACAC GTGTGGAAGG GTCGACAGGA
610 620 630 640 650 660
GCAGTCTGAC CTCTACACTC TGAGCAGCTC AGTGACTGTC CCCTCCAGCA CCTGGCCCAG
CGTCAGACTG GAGATGTGAG ACTCGTCGAG TCACTGACAG GGGAGGTCGT GGACCGGGTC
670 680 690 700 710 720
CGAGACCGTC ACCTGCAACG TTGCCCACCC GGCCAGCAGC ACCAAGGTGG ACAAGAAAAT
GCTCTGGCAG TGGACGTTGC AACGGGTGGG CCGGTCGTCG TGGTTCCACC TGTTCTTTTA
730
TGTGCCCAGG GATTGT 3'
ACACGGGTCC CTAACA 5'

Fig. 4F
Junghans

*** INPUT INFORMATION ***

FILE NAME : 4D4LCDNA.SEQ

SEQUENCE : 504BP; 120 A; 126 C; 122 G; 136 T.

*** SEQUENCE LIST ***

(DOUBLE)

	10	20	30	40	50	60
5'	CTCAAAATGA	AGTTGCCTGT	TAGGCTGTTG	GTGCTGATGT	TCTGGATTCC	TGCTTCCAAC
3'	GAGTTTTACT	TCAACGGACA	ATCCGACAAC	CACGACTACA	AGACCTAAGG	ACGAAGGTTG
	70	80	90	100	110	120
	AGTGATGTTT	TGATGACCCA	ATCTCCACTC	TCCCTGCCTG	TCAGTCTTGG	AGATCAAGCC
	TCACTACAAA	ACTACTGGGT	TAGAGGTGAG	AGGGACGGAC	AGTCAGAACC	TCTAGTTCGG
	130	140	150	160	170	180
	TCCATCTCTT	GCAGATCTAG	TCAGAGCATT	GTCCATAGTA	ATGGAGACAC	CTATTTAGAA
	AGGTAGAGAA	CGTCTAGATC	AGTCTCGTAA	CAGGTATCAT	TACCTCTGTG	GATAAATCTT
	190	200	210	220	230	240
	TGGTACCTGC	AGAAACCAGG	CCAGTCTCCA	AAGCTCCTGA	TCTACAAGGT	TTCCGACCGA
	ACCATGGACG	TCTTTGGTCC	GGTCAGAGGT	TTCGAGGACT	AGATGTTCCA	AAGGCTGGCT
	250	260	270	280	290	300
	TTTTCTGGGG	TCCCAGACAG	GTTCACTGGC	AGTGGATCAG	GGACAGATTT	CACACTCAAG
	AAAAGACCCC	AGGGTCTGTC	CAAGTCACCG	TCACCTAGTC	CCTGTCTAAA	GTGTGAGTTC
	310	320	330	340	350	360
	ATCAGCAGAG	TGGAGGCTGA	GGATCTGGGA	GTTTATTTCT	GCTTTCAAGG	TTCACATGTT
	TAGTCGTCTC	ACCTCCGACT	CCTAGACCCT	CAAATAAAGA	CGAAAGTTCC	AAGTGTACAA
	370	380	390	400	410	420
	CCGTACGCGT	TCGGAGGGGG	GACCAAGCTG	GAAATAAAAC	GGGCTGATGC	TGCACCAACT
	GGCATGCGCA	AGCCTCCCCC	CTGGTTCGAC	CTTTATTTTG	CCCGACTACG	ACGTGGTTGA
	430	440	450	460	470	480
	GTATCCATCT	TCCCACCATC	CAGTGAGCAG	TTAACATCTG	GAGGTGCCTC	AGTCGTGTGC
	CATAGGTAGA	AGGGTGGTAG	GTCACCTCGT	AATTGTAGAC	CTCCACGGAG	TCAGCACACG
	490	500				
	TTCTTGAACA	ACTTCTACCC	CAAA	3'		
	AAGAACTTGT	TGAAGATGGG	GTTT	5'		

Fig. 49
Jurahans

*** INPUT INFORMATION ***

FILE NAME : 3E11HCDN.SEQ

SEQUENCE : 761BP; 167 A; 213 C; 188 G; 193 T.

*** SEQUENCE LIST ***

(DOUBLE)

	10	20	30	40	50	60
5'	CCTGGATTCA	ATTTCCAGTT	CCTCACATTC	AGTGATCAGC	ACTGAACACG	GACCCCTCAC
3'	GGACCTAAGT	TAAAGGTCAA	GGAGTGTAAG	TCACTAGTCG	TGACTTGTGC	CTGGGGAGTG
	70	80	90	100	110	120
	CATGAACTTC	GGGCTCAGCT	TGATTTTCCT	TGTCCTTGTT	TTAAAAGGTG	TCCAGTGTGA
	GTACTTGAAG	CCCGAGTCGA	ACTAAAAGGA	ACAGGAACAA	AATTTTCCAC	AGGTCACACT
	130	140	150	160	170	180
	AGTGAAACTG	GTGGAGTCTG	GGGGAGACTT	AATGAACCCT	GGAGCGTCTC	TGAAACTCTC
	TCACCTTGAC	CACCTCAGAC	CCCCCTCTGA	TTACTTGGGA	CCTCGCAGAG	ACTTTGAGAG
	190	200	210	220	230	240
	CTGTGCAGCC	TCTGGATTCA	GTTTCAGTAA	CTATGGCATG	TCTTGGGTTC	GCCAGACTTC
	GACACGTCGG	AGACCTAAGT	CAAAGTCATT	GATACCGTAC	AGAACCCAAG	CGGTCTGAAG
	250	260	270	280	290	300
	AGACAAGAGG	CTGGAGTGGG	TCGCTTCCAT	TAGTACGGGT	GGTGCTAATA	CCTTCTATCC
	TCTGTTCTCC	GACCTCACCC	AGCGAAGGTA	ATCATGCCCA	CCACGATTAT	GGAAGATAGG
	310	320	330	340	350	360
	AGACAATGTA	AAGGGCCGAT	TCACCATTTC	CAGAGAGAAT	GCCAAGAACA	CCCTATACCT
	TCTGTTACAT	TTCCCGGCTA	AGTGGTAAAG	GTCTCTCTTA	CGGTTCTTGT	GGGATATGGA
	370	380	390	400	410	420
	GCAAATGAGT	AGTCTGAAGT	CTGAGGACAC	GGCCTTGAT	TTCTGTGCAA	GAGATAGTCA
	CGTTTACTCA	TCAGACTTCA	GACTCCTGTG	CCGGAACATA	AAGACACGTT	CTCTATCAGT
	430	440	450	460	470	480
	CTCCGTAGGT	TGTTGGTTTG	CTACCTGGGG	CCAAGGGACT	CTGGTCACTG	TCTCTGCAGC
	GAGGCATCCA	ACAACCAAAC	GATGGACCCC	GGTTCCCTGA	GACCAGTGAC	AGAGACGTCG
	490	500	510	520	530	540
	CAAAACAACA	CCCCCATCAG	TCTATCCACT	GGCCCCCTGG	TGTGGAGATA	CTACTGGTTC
	GTTTTGTGTG	GGGGGTAGTC	AGATAGGTGA	CCGGGGACCC	ACACCTCTAT	GATGACCAAG
	550	560	570	580	590	600
	CTCCGTGACT	CTGGGATGCC	TGGTCAAGGG	CTACTTCCCT	GAGTCAGTGA	CTGTGACTTG
	GAGGCACTGA	GACCCTACGG	ACCAGTTCCC	GATGAAGGGA	CTCAGTCACT	GACACTGAAC
	610	620	630	640	650	660
	GAACTCCGGA	TCCCTGCCCA	GCAGTGTGCA	CACCTTCCCA	GCTCTCCTGC	AGTCTGGACT
	CTTGAGGCCT	AGGGACGGGT	CGTCACACGT	GTGGAAGGGT	CGAGAGGACG	TCAGACCTGA
	670	680	690	700	710	720
	CTACACTATG	AGCAGCTCAG	TGACTGTCCC	CTCCAGCACC	TGGCCAAGCC	AGACCGTTAC
	GATGTGATAC	TCGTCGAGTC	ACTGACAGGG	GAGGTCGTGG	ACCGGTTCCG	TCTGGCAATG
	730	740	750	760		
	CTGCAGTGTT	GCTCACCCAG	CCAGCAGCAC	CACGGTGGAC	A 3'	
	GACGTCACAA	CGAGTGGGTC	GGTCGTCGTG	GTGCCACCTG	T 5'	

Fig. 4H
Junghans

*** INPUT INFORMATION ***

FILE NAME : 3E11LCDN.SEQ

SEQUENCE : 698BP; 199 A; 179 C; 167 G; 153 T.

*** SEQUENCE LIST ***

(DOUBLE)

10	20	30	40	50	60
5' CCAGCATGGG	CATCAAGATG	GAATCACAGA	CTCTGGTCTT	CATATCCATA	CTGCTCTGGT
3' GGTCGTACCC	GTAGTTCTAC	CTTAGTGTCT	GAGACCAGAA	GTATAGGTAT	GACGAGACCA
70	80	90	100	110	120
TATATGGAGC	TGATGGGAAC	ATTGTAATGA	CCCAATCTCC	CAAATCCATG	TCCATGTCAG
ATATACCTCG	ACTACCCTTG	TAACATTACT	GGGTTAGAGG	GTTTAGGTAC	AGGTACAGTC
130	140	150	160	170	180
TAGGAGAGAG	GGTCACCTTG	ACCTGCAAGG	CCAGTGAGAA	TGTGGTTACT	TATGTTTCCT
ATCCTCTCTC	CCAGTGGAAC	TGGACGTTCC	GGTCACTCTT	ACACCAATGA	ATACAAAGGA
190	200	210	220	230	240
GGTATCAACA	GAAACCAGAG	CAGTCTCCTA	AACTGCTGAT	ATACGGGGCA	TCCAACCGGT
CCATAGTTGT	CTTTGGTCTC	GTCAGAGGAT	TTGACGACTA	TATGCCCCGT	AGGTTGGCCA
250	260	270	280	290	300
ACACTGGGGT	CCCCGATCGC	TTCACAGGCA	GTGGATCTGC	AACAGATTTT	ACTCTGACCA
TGTGACCCCA	GGGGCTAGCG	AAGTGTCCGT	CACCTAGACG	TTGTCTAAAG	TGAGACTGGT
310	320	330	340	350	360
TCAGCAGTGT	GCAGGCTGAA	GACCTTGCAG	ATTATCACTG	TGGACAGGGT	TACAGCTATC
AGTCGTCACA	CGTCCGACTT	CTGGAACGTC	TAATAGTGAC	ACCTGTCCCA	ATGTCGATAG
370	380	390	400	410	420
CGTACACGTT	CGGAGGGGGG	ACCAAGCTGG	AAATAAAACG	GGCTGATGCT	GCACCAACTG
GCATGTGCAA	GCCTCCCCCC	TGGTTCGACC	TTTATTTTGC	CCGACTACGA	CGTGGTTGAC
430	440	450	460	470	480
TATCCATCTT	CCCACCATCC	AGTGAGCAGT	TAACATCTGG	AGGTGCCTCA	GTCGTGTGCT
ATAGGTAGAA	GGGTGGTAGG	TCACTCGTCA	ATTGTAGACC	TCCACGGAGT	CAGCACACGA
490	500	510	520	530	540
TCTTGAACAA	CTTCTACCCC	AAAGACATCA	ATGTCAAGTG	GAAGATTGAT	GGCAGTGAAC
AGAACTTGTT	GAAGATGGGG	TTTCTGTAGT	TACAGTTCAC	CTTCTAACTA	CCGTCACCTG
550	560	570	580	590	600
GACAAAATGG	CGTCCTGAAC	AGTTGGACTG	ATCAGGACAG	CAAAGACAGC	ACCTACAGCA
CTGTTTTTACC	GCAGGACTTG	TCAACCTGAC	TAGTCCTGTC	GTTTCTGTCT	TGGATGTCGT
610	620	630	640	650	660
TGAGCAGCAC	CCTCACGTTG	ACCAAGGACG	AGTATGAACG	ACATAACAGC	TATACCTGTG
ACTCGTCGTG	GGAGTGCAAC	TGGTTCCTGC	TCATACTTGC	TGTATTGTCT	ATATGGACAC
670	680	690			
AGGCCACTCA	CAAGACATCA	ACTTCACCCA	TCGTCAAG	3'	
TCCGGTGAGT	GTTCTGTAGT	TGAAGTGGGT	AGCAGTTC	5'	

Fig. 4I
Jungkins

Anti-GD3 IgTCR-modified T cells

Anti-Melanoma IgTCR Tumor Targeting

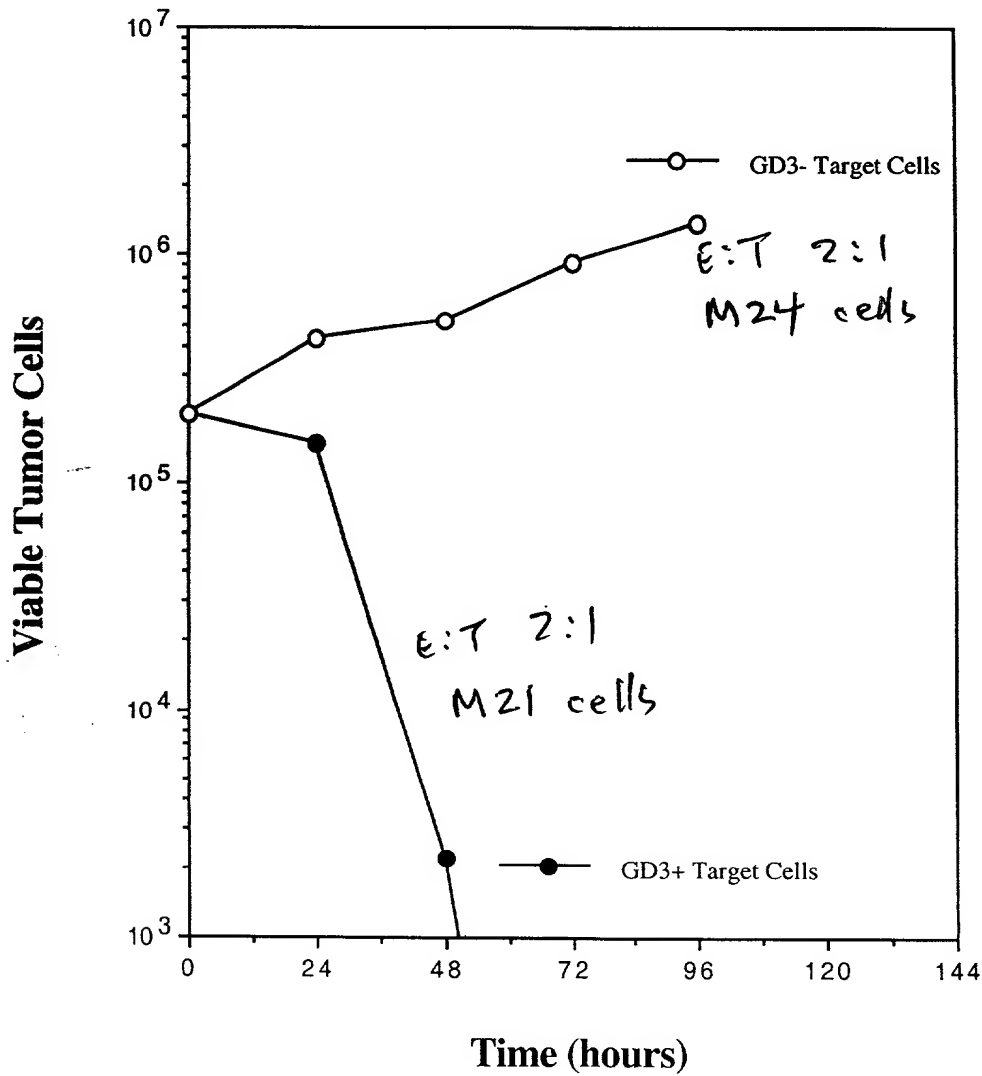


Fig. 5
Jung et al.

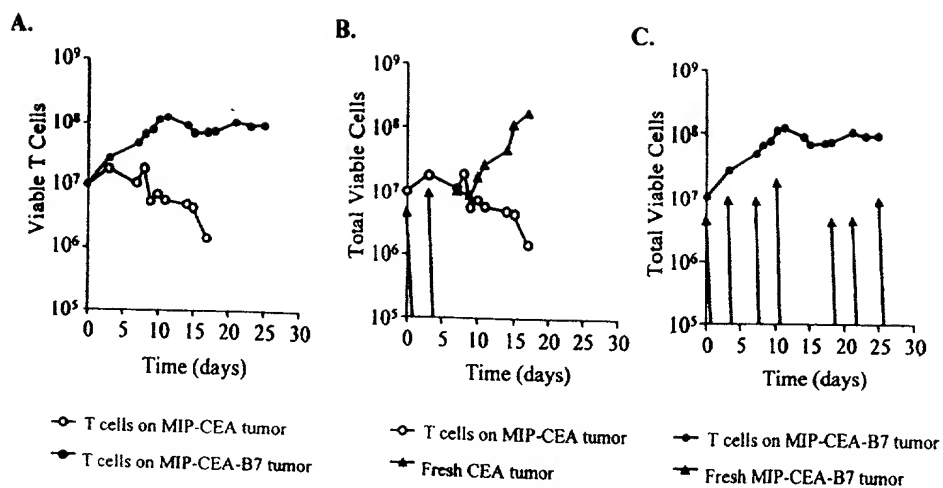


Fig. 6
Jungmans

CD28, IgCD28, and IgTCR

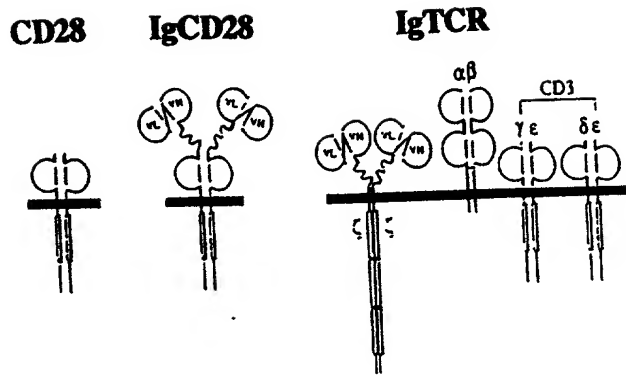


Fig. 7
Singhans